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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/658,884

DATE: 10/15/2004

TIME: 12:39:31

Input Set : N:\Crf4\Refhold\10_folder\J658884.raw

Output Set: N:\CRF4\10152004\J658884.raw

SEQUENCE LISTING

1 (1) GENERAL INFORMATION:

2 (i) APPLICANT: Bandman, Olga
3 Goli, Surya K.

4 (ii) TITLE OF INVENTION: NOVEL HUMAN MAGE-LIKE PROTEIN

5 (iii) NUMBER OF SEQUENCES: 6

6 (iv) CORRESPONDENCE ADDRESS:

7 (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
8 (B) STREET: 3174 Porter Drive
9 (C) CITY: Palo Alto
10 (D) STATE: CA
11 (E) COUNTRY: USA
12 (F) ZIP: 94304

13 (v) COMPUTER READABLE FORM:

14 (A) MEDIUM TYPE: Diskette
15 (B) COMPUTER: IBM Compatible
16 (C) OPERATING SYSTEM: DOS
17 (D) SOFTWARE: FastSEQ for Windows Version 2.0

18 (vi) CURRENT APPLICATION DATA:

C--> 19 (A) APPLICATION NUMBER: US/10/658,884
C--> 20 (B) FILING DATE: 09-Sep-2003

21 (C) CLASSIFICATION: 435

22 (vii) PRIOR APPLICATION DATA:

23 (A) APPLICATION NUMBER: US/08/773,870
24 (B) FILING DATE: 27-DEC-1996

25 (viii) ATTORNEY/AGENT INFORMATION:

26 (A) NAME: Billings, Lucy J.
27 (B) REGISTRATION NUMBER: 36,749
28 (C) REFERENCE/DOCKET NUMBER: PF-0179 US

29 (ix) TELECOMMUNICATION INFORMATION:

30 (A) TELEPHONE: 415-855-0555
31 (B) TELEFAX: 415-845-4166
32 (C) TELEX:

33 (2) INFORMATION FOR SEQ ID NO: 1:

34 (i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 411 amino acids
36 (B) TYPE: amino acid
37 (C) STRANDEDNESS: single
38 (D) TOPOLOGY: linear

39 (vii) IMMEDIATE SOURCE:

40 (A) LIBRARY: Consensus
41 (B) CLONE: Consensus

42 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ENTERED

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W--> 43 Met Ala Phe Pro Arg Pro Lys Lys Asn Leu Pro Gln Pro Lys Xaa Ala
44 1 5 10 15
45 Ala Thr Glu Gly Pro Ser Ala Ala Ser Gly Val Pro Gln Thr Gly Pro
46 20 25 30
47 Gly Arg Glu Val Ala Ala Thr Arg Pro Lys Thr Thr Lys Ser Gly Lys
48 35 40 45
49 Ala Leu Ala Lys Thr Arg Trp Val Glu Pro Gln Asn Val Val Ala Ala
50 50 55 60
51 Ala Ala Ala Lys Ala Lys Met Ala Thr Ser Ile Pro Glu Pro Glu Gly
52 65 70 75 80
53 Ala Ala Ala Ala Thr Ala Gln His Ser Ala Glu Pro Trp Ala Arg Met
54 85 90 95
55 Gly Gly Lys Arg Thr Lys Lys Ser Lys His Leu Asp Asp Glu Tyr Glu
56 100 105 110
57 Ser Ser Glu Glu Glu Arg Glu Thr Pro Ala Val Pro Pro Thr Trp Arg
58 115 120 125
59 Ala Ser Gln Pro Ser Leu Thr Val Arg Ala Gln Leu Ala Pro Arg Pro
60 130 135 140
61 Pro Met Ala Pro Arg Ser Gln Ile Pro Ser Arg His Val Leu Cys Leu
62 145 150 155 160
63 Pro Pro Arg Asn Val Thr Leu Leu Gln Glu Arg Ala Asn Lys Leu Val
64 165 170 175
65 Lys Tyr Leu Met Ile Lys Asp Tyr Lys Lys Ile Pro Ile Lys Arg Ala
66 180 185 190
67 Asp Met Leu Lys Asp Val Ile Arg Glu Tyr Asp Glu His Phe Pro Glu
68 195 200 205
69 Ile Ile Glu Arg Ala Thr Tyr Thr Leu Glu Lys Lys Phe Gly Ile His
70 210 215 220
71 Leu Lys Glu Ile Asp Lys Glu Glu His Leu Tyr Ile Leu Val Cys Thr
72 225 230 235 240
73 Arg Asp Ser Ser Ala Arg Leu Leu Gly Lys Thr Lys Asp Thr Pro Arg
74 245 250 255
75 Leu Ser Leu Leu Val Ile Leu Gly Val Ile Phe Met Asn Gly Asn
76 260 265 270
77 Arg Ala Ser Glu Ala Val Leu Trp Glu Ala Leu Arg Lys Met Gly Leu
78 275 280 285
79 Arg Pro Gly Val Arg His Pro Leu Leu Gly Asp Leu Arg Lys Leu Leu
80 290 295 300
81 Thr Tyr Glu Phe Val Lys Gln Lys Tyr Leu Asp Tyr Arg Arg Val Pro
82 305 310 315 320
83 Asn Ser Asn Pro Pro Glu Tyr Glu Phe Leu Trp Gly Leu Arg Ser Tyr
84 325 330 335
85 His Glu Thr Ser Lys Met Lys Val Leu Arg Phe Ile Ala Glu Val Gln
86 340 345 350
87 Lys Arg Asp Pro Arg Asp Trp Thr Ala Gln Phe Met Glu Ala Ala Asp
88 355 360 365
89 Glu Ala Leu Asp Ala Leu Asp Ala Ala Ala Glu Ala Glu Ala Arg
90 370 375 380
91 Ala Glu Ala Arg Thr Arg Met Gly Ile Gly Asp Glu Ala Val Ser Gly

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92 385 390 395 400
 93 Pro Gly Ala Gly Met Thr Leu Ser Leu Ser Cys
 94 405 410
 96 (2) INFORMATION FOR SEQ ID NO: 2:
 97 (i) SEQUENCE CHARACTERISTICS:
 98 (A) LENGTH: 1247 base pairs
 99 (B) TYPE: nucleic acid
 100 (C) STRANDEDNESS: single
 101 (D) TOPOLOGY: linear
 102 (vii) IMMEDIATE SOURCE:
 103 (A) LIBRARY: Consensus
 104 (B) CLONE: Consensus
 105 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 106 CNACGNGAAT GGCCCTCCCC CGCCCCAAGA AGAACCTGCC CCAGCCCAAG NAGGCTGCCA 60
 107 CAGAGGGCCC CAGTGCTGCC TCTGGTGTGC CCCAGACGGG ACCTGGCAGG GAGGTGGCAG 120
 108 CCACCCGGCC CAAGACCACC AAGTCGGGGA AGGCGCTGGC CAAGACTCGG TGGGTGGAGC 180
 109 CTCAGAATGT TGTGGCAGCA GCTGCTGCCA AGGCCAAGAT GGCCACGAGC ATCCCTGAGC 240
 110 CGGAGGGTGC AGCTGCTGCC ACTGCTCAGC ACAGTGCTGA GCCCTGGGCC AGGATGGGAG 300
 111 GCAAGAGGAC CAAGAAGTCC AAGCACCTGG ATGATGAGTA TGAGAGCAGC GAGGAGGAGA 360
 112 GAGAGACTCC CGCGGTCCCA CCCACCTGGA GAGCATCACA GCCCTCATTG ACGGTGCGGG 420
 113 CTCAGTTGGC CCCTCGGGCC CCGATGGCCC CGAGGTCCCA GATAACCTCA AGGCACGTAC 480
 114 TGTGCCTGCC CCCCCGCAAC GTGACCCCTTC TGCAAGGAGAG GGCAAATAAG TTGGTGAAT 540
 115 ACCTGATGAT TAAGGACTAC AAGAAGATCC CCATCAAGCG CGCAGACATG CTGAAGGATG 600
 116 TCATCAGAGA ATATGATGAA CATTTCCTG AGATCATTGA ACGAGCAACG TACACCCCTGG 660
 117 AAAAGAAGTT TGGGATCCAC CTGAAGGAGA TCGACAAGGA AGAACACCTG TATATTCTTG 720
 118 TCTGCACACG GGACTCCTCA GCTCGCCTCC TTGGAAAAAC CAAGGACACT CCCAGGCTGA 780
 119 GTCTCCTCTT GGTGATTCTG GGCCTCATCT TCATGAATGG CAACCGTGCC AGCGAGGCTG 840
 120 TCCTCTGGGA GGCCTACACG AAGATGGGAC TGCGTCCTGG GGTGAGACAT CCCCTCCTTG 900
 121 GAGATCTAAG GAAACTTCTC ACCTATGAGT TTGTAAAGCA GAAATACTG GACTACAGAC 960
 122 GAGTCCCCAA CAGCAACCCC CCGGAGTATG AGTTCCCTCTG GGGCCTCCGT TCCTACCATG 1020
 123 AGACTAGCAA GATGAAAGTG CTGAGATTCA TTGCAGAGGT TCAGAAAAGA GACCCTCGTG 1080
 124 ACTGGACTGC ACAGTTCATG GAGGCTGCAG ATGAGGCCTT GGATGCTCTG GATGCTGCTG 1140
 125 CAGCTGAGGC CGAAGCCCCG GCTGAAGCAA GAACCCGCAT GGGATTGGA GATGAGGCTG 1200
 126 TGTCTGGGCC CGGAGCTGGG ATGACATTGA GTTGAGCTG CTGACCT 1247
 128 (2) INFORMATION FOR SEQ ID NO: 3:
 129 (i) SEQUENCE CHARACTERISTICS:
 130 (A) LENGTH: 347 amino acids
 131 (B) TYPE: amino acid
 132 (C) STRANDEDNESS: single
 133 (D) TOPOLOGY: linear
 134 (vii) IMMEDIATE SOURCE:
 135 (A) LIBRARY: GenBank
 136 (B) CLONE: 608993
 137 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 138 Met Pro Arg Gly Gln Lys Ser Lys Leu Arg Ala Arg Glu Lys Arg Arg
 139 1 5 10 15
 140 Lys Ala Arg Glu Glu Thr Gln Gly Leu Lys Val Arg His Ala Thr Ala
 141 20 25 30
 142 Ala Glu Lys Glu Glu Cys Pro Ser Ser Pro Val Leu Gly Asp Thr

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143 35 40 45
 144 Pro Thr Ser Ser Pro Ala Ala Gly Ile Pro Gln Lys Pro Gln Gly Ala
 145 50 55 60
 146 Pro Pro Thr Thr Thr Ala Ala Ala Ala Val Ser Cys Thr Glu Ser Asp
 147 65 70 75 80
 148 Glu Gly Ala Lys Cys Gln Gly Glu Glu Asn Ala Ser Phe Ser Gln Ala
 149 85 90 95
 150 Thr Thr Ser Thr Glu Ser Ser Val Lys Asp Pro Val Ala Trp Glu Ala
 151 100 105 110
 152 Gly Met Leu Met His Phe Ile Leu Arg Lys Tyr Lys Met Arg Glu Pro
 153 115 120 125
 154 Ile Met Lys Ala Asp Met Leu Lys Val Val Asp Glu Lys Tyr Lys Asp
 155 130 135 140
 156 His Phe Thr Glu Ile Leu Asn Gly Ala Ser Arg Arg Leu Glu Leu Val
 157 145 150 155 160
 158 Phe Gly Leu Asp Leu Lys Glu Asp Asn Pro Ser Ser His Thr Tyr Thr
 159 165 170 175
 160 Leu Val Ser Lys Leu Asn Leu Thr Asn Asp Gly Asn Leu Ser Asn Asp
 161 180 185 190
 162 Trp Asp Phe Pro Arg Asn Gly Leu Leu Met Pro Leu Leu Gly Val Ile
 163 195 200 205
 164 Phe Leu Lys Gly Asn Ser Ala Thr Glu Glu Glu Ile Trp Lys Phe Met
 165 210 215 220
 166 Asn Val Leu Gly Ala Tyr Asp Gly Glu Glu His Leu Ile Tyr Gly Glu
 167 225 230 235 240
 168 Pro Arg Lys Phe Ile Thr Gln Asp Leu Val Gln Glu Lys Tyr Leu Lys
 169 245 250 255
 170 Tyr Glu Gln Val Pro Asn Ser Asp Pro Pro Arg Tyr Gln Phe Leu Trp
 171 260 265 270
 172 Gly Pro Arg Ala Tyr Ala Glu Thr Thr Lys Met Lys Val Leu Glu Phe
 173 275 280 285
 174 Leu Ala Lys Met Asn Gly Ala Thr Pro Arg Asp Phe Pro Ser His Tyr
 175 290 295 300
 176 Glu Glu Ala Leu Arg Asp Glu Glu Glu Arg Ala Gln Val Arg Ser Ser
 177 305 310 315 320
 178 Val Arg Ala Arg Arg Arg Thr Thr Ala Thr Thr Phe Arg Ala Arg Ser
 179 325 330 335
 180 Arg Ala Pro Phe Ser Arg Ser Ser His Pro Met
 181 340 345
 183 (2) INFORMATION FOR SEQ ID NO: 4:
 184 (i) SEQUENCE CHARACTERISTICS:
 185 (A) LENGTH: 369 amino acids
 186 (B) TYPE: amino acid
 187 (C) STRANDEDNESS: single
 188 (D) TOPOLOGY: linear
 189 (vii) IMMEDIATE SOURCE:
 190 (A) LIBRARY: GenBank
 191 (B) CLONE: 533511
 192 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

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193 Met Pro Arg Ala Pro Lys Arg Gln Arg Cys Met Pro Glu Glu Asp Leu
194 1 5 10 15
195 Gln Ser Gln Ser Glu Thr Gln Gly Leu Glu Gly Ala Gln Ala Pro Leu
196 20 25 30
197 Ala Val Glu Glu Asp Ala Ser Ser Ser Thr Ser Thr Ser Ser Ser Phe
198 35 40 45
199 Pro Ser Ser Phe Pro Ser Ser Ser Ser Ser Ser Ser Cys Tyr
200 50 55 60
201 Pro Leu Ile Pro Ser Thr Pro Glu Glu Val Ser Ala Asp Asp Glu Thr
202 65 70 75 80
203 Pro Asn Pro Pro Gln Ser Ala Gln Ile Ala Cys Ser Ser Pro Ser Val
204 85 90 95
205 Val Ala Ser Leu Pro Leu Asp Gln Ser Asp Glu Gly Ser Ser Ser Gln
206 100 105 110
207 Lys Glu Glu Ser Pro Ser Thr Leu Gln Val Leu Pro Asp Ser Glu Ser
208 115 120 125
209 Leu Pro Arg Ser Glu Ile Asp Glu Lys Val Thr Asp Leu Val Gln Phe
210 130 135 140
211 Leu Leu Phe Lys Tyr Gln Met Lys Glu Pro Ile Thr Lys Ala Glu Ile
212 145 150 155 160
213 Leu Glu Ser Val Ile Lys Asn Tyr Glu Asp His Phe Pro Leu Leu Phe
214 165 170 175
215 Ser Glu Ala Ser Glu Cys Met Leu Leu Val Phe Gly Ile Asp Val Lys
216 180 185 190
217 Glu Val Asp Pro Thr Gly His Ser Phe Val Leu Val Thr Ser Leu Gly
218 195 200 205
219 Leu Thr Tyr Asp Gly Met Leu Ser Asp Val Gln Ser Met Pro Lys Thr
220 210 215 220
221 Gly Ile Leu Ile Leu Ile Leu Ser Ile Ile Phe Ile Glu Gly Tyr Cys
222 225 230 235 240
223 Thr Pro Glu Glu Val Ile Trp Glu Ala Leu Asn Met Met Gly Leu Tyr
224 245 250 255
225 Asp Gly Met Glu His Leu Ile Tyr Gly Glu Pro Arg Lys Leu Leu Thr
226 260 265 270
227 Gln Asp Trp Val Gln Glu Asn Tyr Leu Glu Tyr Arg Gln Val Pro Gly
228 275 280 285
229 Ser Asp Pro Ala Arg Tyr Glu Phe Leu Trp Gly Pro Arg Ala His Ala
230 290 295 300
231 Glu Ile Arg Lys Met Ser Leu Leu Lys Phe Leu Ala Lys Val Asn Gly
232 305 310 315 320
233 Ser Asp Pro Arg Ser Phe Pro Leu Trp Tyr Glu Glu Ala Leu Lys Asp
234 325 330 335
235 Glu Glu Glu Arg Ala Gln Asp Arg Ile Ala Thr Thr Asp Asp Thr Thr
236 340 345 350
237 Ala Met Ala Ser Ala Ser Ser Ala Thr Gly Ser Phe Ser Tyr Pro
238 355 360 365
239 Glu
241 (2) INFORMATION FOR SEQ ID NO: 5:
242 (i) SEQUENCE CHARACTERISTICS: